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Reviewer: Anne Corrigan

Timestamp: [year=2008; month=8; day=13; hr=9; min=22; sec=53; ms=21; ]

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Sequence Listing was accepted.

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217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=8; day=11; hr=17; min=28; sec=25; ms=669; ]

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Application No: 10591752 Version No: 2.0

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# SEQUENCE LISTING

<110> YOKOTA, Akiho  
 SHIGEOKA, Shigeru  
 TOMIZAWA, Ken-ichi

<120> METHOD FOR IMPROVING PRODUCTIVITY OF PLANT BY CHLOROPLAST  
 TECHNOLOGY

<130> 2006\_1303A

<140> 10591752  
 <141> 2008-07-09

<150> PCT/JP2005/004037  
 <151> 2005-03-02

<150> JP 2004-059513  
 <151> 2004-03-03

<160> 18

<170> PatentIn version 3.4

<210> 1  
 <211> 358  
 <212> PRT  
 <213> Spinacia oleracea L

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<223> Fructose-1,6-bisphosphatase

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 20 25 30

Ala Gly Val Ile Asp Ala Glu Leu Thr Ile Val Leu Ser Ser Ile Ser  
 35 40 45

Leu Ala Cys Lys Gln Ile Ala Ser Leu Val Gln Arg Ala Gly Ile Ser  
 50 55 60

Asn Leu Thr Gly Ile Gln Gly Ala Val Asn Ile Gln Gly Glu Asp Gln  
 65 70 75 80

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Asn	Tyr	Lys	Met	Trp	Asp	Asp	Lys	Leu	Lys	Lys	Tyr	Met	Asp	Asp	Leu	
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Tyr	Glu	Cys	Ala	Pro	Met	Ser	Phe	Ile	Val	Glu	Gln	Ala	Gly	Gly	Lys	

305 310 315 320

Gly Ser Asp Gly His Gln Arg Ile Leu Asp Ile Gln Pro Thr Glu Ile  
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Leu Glu Lys Tyr Leu Ala  
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<213> Spinacia oleracea L

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<223> Fructose-1,6-bisphosphatase

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accatcgttc tttctagcat ttcattggct tgtaaacaaa ttgcttcctt gggtcaacga 180  
gctgggtatatt ctaacttgac tggaattcaa ggtgctgtca atatccaagg agaggatcag 240  
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<210> 3

<211> 333

<212> PRT

<213> Spinacia oleracea L

<220>

<223> Sedoheptulose-1, 7-bisphosphatase

<400> 3

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Ile	Arg	Leu	Met	Met	Cys	Met	Gly	Glu	Ala	Leu	Arg	Thr	Ile	Gly	Phe
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Lys	Val	Arg	Thr	Ala	Ser	Cys	Gly	Gly	Thr	Gln	Cys	Val	Asn	Thr	Phe
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Gly	Asp	Glu	Gln	Leu	Ala	Ile	Asp	Val	Leu	Ala	Asp	Lys	Leu	Leu	Phe
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Glu	Ala	Leu	Asn	Tyr	Ser	His	Phe	Cys	Lys	Tyr	Ala	Cys	Ser	Glu	Glu
			85						90					95	
Leu	Pro	Glu	Leu	Gln	Asp	Met	Gly	Gly	Pro	Val	Asp	Gly	Gly	Phe	Ser
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Val	Ala	Phe	Asp	Pro	Leu	Asp	Gly	Ser	Ser	Ile	Val	Asp	Thr	Asn	Phe
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Ser	Val	Gly	Thr	Ile	Phe	Gly	Val	Trp	Pro	Gly	Asp	Lys	Leu	Thr	Gly
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145					150					155					160

Arg Thr Thr Tyr Val Leu Ala Leu Lys Asp Tyr Pro Gly Thr His Glu  
165 170 175

Phe Leu Leu Leu Asp Glu Gly Lys Trp Gln His Val Lys Glu Thr Thr  
180 185 190

Glu Ile Asn Glu Gly Lys Leu Phe Cys Pro Gly Asn Leu Arg Ala Thr  
195 200 205

Ser Asp Asn Ala Asp Tyr Ala Lys Leu Ile Gln Tyr Tyr Ile Lys Glu  
210 215 220

Lys Tyr Thr Leu Arg Tyr Thr Gly Gly Met Val Pro Asp Val Asn Gln  
225 230 235 240

Ile Ile Val Lys Glu Lys Gly Ile Phe Thr Asn Val Ile Ser Pro Thr  
245 250 255

Ala Lys Ala Lys Leu Arg Leu Leu Phe Glu Val Ala Pro Leu Gly Phe  
260 265 270

Leu Ile Glu Lys Ala Gly Gly His Ser Ser Glu Gly Thr Lys Ser Val  
275 280 285

Leu Asp Ile Glu Val Lys Asn Leu Asp Asp Arg Thr Gln Val Ala Tyr  
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Gly Ser Leu Asn Glu Ile Ile Arg Phe Glu Lys Thr Leu Tyr Gly Ser  
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325 330

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<212> DNA  
<213> Spinacia oleracea L

<220>

<223> Sedoheptulose-1,7-bisphosphatase

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gaagcattaa ggaccattgg ctttaaagtg aggactgctt catgtggtgg aactcaatgt 180

gttaacacct ttggagacga acagcttgcc attgatgtgc ttgctgacaa gcttccttttc 240

gaggcattga actattcaca cttctgcaag tatgcttggt cagaagaact ccctgagctt 300

caagatatgg gagggccccgt tgatggcgga ttcagtgtag catttgaccc ccttgatgga 360

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aagctaactg gtgtaacagg cagagatcaa gtggctgctg caatgggaat ttatggtcct 480

aggactactt atgttctcgc tcttaaggac taccctggca cccatgaatt tcttccttctt 540

gatgaaggaa agtggcaaca tgtgaaagaa acaacagaaa tcaatgaagg aaaattgttc 600

tgtcctggaa acttgagagc cacttctgac aatgctgatt atgctaagct gattcaatac 660

tatataaaag agaaatacac attgagatac actggaggaa tggttcctga tgtaaccag 720

atcatagtga aggagaaagg tatattcaca aatgtaatat cacctacagc caaggcaaag 780

ttgaggttac tgtttgaggt agctcctcta gggttcttga ttgagaaggc tggtggtcac 840

agcagtgagg gaaccaagtc tgtgttggaac attgaagtca aaaaccttga tgacagaacc 900

caagttgctt acggctcctt gaacgagatc atccgatttg agaagacact atacggatcc 960

tctaggctag aggagccagt tcctggtgga gctgctgct 999

<210> 5

<211> 356

<212> PRT

<213> Synechococcus

<220>

<223> fructose-1,6-bisphosphatase/sedoheptulose-1,7-bisphosphatase from  
Synechococcus PCC 7942

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Ala Ile Ala Ser Ala Arg Leu Met Gly Lys Gly Glu Lys Asn Glu Ala  
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Asp Arg Val Ala Val Glu Ala Met Arg Val Arg Met Asn Gln Val Glu  
35 40 45

Met Leu Gly Arg Ile Val Ile Gly Glu Gly Glu Arg Asp Glu Ala Pro  
50 55 60

Met Leu Tyr Ile Gly Glu Glu Val Gly Ile Tyr Arg Asp Ala Asp Lys  
65 70 75 80

Arg Ala Gly Val Pro Ala Gly Lys Leu Val Glu Ile Asp Ile Ala Val  
85 90 95

Asp Pro Cys Glu Gly Thr Asn Leu Cys Ala Tyr Gly Gln Pro Gly Ser  
100 105 110

Met Ala Val Leu Ala Ile Ser Glu Lys Gly Gly Leu Phe Ala Ala Pro  
115 120 125

Asp Phe Tyr Met Lys Lys Leu Ala Ala Pro Pro Ala Ala Lys Gly Lys  
130 135 140

Glu Thr Ser Ile Lys Ser Ala Thr Glu Asn Leu Lys Ile Leu Ser Glu  
145 150 155 160

Cys Leu Asp Arg Ala Ile Asp Glu Leu Val Val Val Val Met Asp Arg  
165 170 175

Pro Arg His Lys Glu Leu Ile Gln Glu Ile Arg Gln Ala Gly Ala Arg  
180 185 190

Val Arg Leu Ile Ser Asp Gly Asp Val Ser Ala Ala Ile Ser Cys Gly  
195 200 205

Phe Ala Gly Thr Asn Thr His Ala Leu Met Gly Ile Gly Ala Ala Pro  
210 215 220

Glu Gly Val Ile Ser Ala Ala Ala Met Arg Cys Leu Gly Gly His Phe  
225 230 235 240

Gln Gly Gln Leu Ile Tyr Asp Pro Glu Val Val Lys Thr Gly Leu Ile  
245 250 255

Gly Glu Ser Arg Glu Ser Asn Ile Ala Arg Leu Gln Glu Met Gly Ile  
260 265 270

Thr Asp Pro Asp Arg Val Tyr Asp Ala Asn Glu Leu Ala Ser Gly Gln  
275 280 285

Glu Val Leu Phe Ala Ala Cys Gly Ile Thr Pro Gly Leu Leu Met Glu  
290 295 300

Gly Val Arg Phe Phe Lys Gly Gly Ala Arg Thr Gln Ser Leu Val Ile  
305 310 315 320

Ser Ser Gln Ser Arg Thr Ala Arg Phe Val Asp Thr Val His Met Phe  
325 330 335

Asp Asp Val Lys Thr Val Ser Leu Pro Leu Ile Pro Asp Pro Lys Trp  
340 345 350

Arg Pro Glu Arg  
355

<210> 6  
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<212> DNA  
<213> Synechococcus

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Synechococcus PCC 7942

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cgagattatt gaagttgtcg agcaggcagc gatcgctctg gcccgctga tgggcaaagg 180  
cgaaaagaat gaagccgatc gcgtcgcagt agaagcgatg cgggtgcgga tgaaccaagt 240  
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caagctggtg gaaatcgaca tcgccgttga ccctgcgaa ggcaccaacc tctgcgccta 420  
cggtcagccc ggctcgatgg cagttttggc catctccgag aaaggcggcc tgtttgcagc 480  
tcccgacttc tacatgaaga aactggctgc acccccagct gccaaaggca aagagacatc 540  
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tgaattggtg gtcgtggtca tggatcgtcc ccgccacaaa gagctaatacc aagagatccg 660  
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<223> psbA promoter

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# SEQUENCE LISTING

<110> YOKOTA, Akiho  
 SHIGEOKA, Shigeru  
 TOMIZAWA, Ken-ichi

<120> METHOD FOR IMPROVING PRODUCTIVITY OF PLANT BY CHLOROPLAST  
 TECHNOLOGY

<130> 2006\_1303A

<140> 10591752  
 <141> 2008-07-09

<150> PCT/JP2005/004037  
 <151> 2005-03-02

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<170> PatentIn version 3.4

<210> 1  
 <211> 358  
 <212> PRT  
 <213> Spinacia oleracea L

<220>

<223> Fructose-1,6-bisphosphatase

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Lys Tyr Glu Ile Glu Thr Leu Thr Gly Trp Leu Leu Lys Gln Glu Met  
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 35 40 45

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 50 55 60

Asn Leu Thr Gly Ile Gln Gly Ala Val Asn Ile Gln Gly Glu Asp Gln  
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Gly	Tyr	Pro	Arg	Asp	Ala	Lys	Ser	Lys	Asn	Gly	Lys	Leu	Arg	Leu	Leu	
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Tyr	Glu	Cys	Ala	Pro	Met	Ser	Phe	Ile	Val	Glu	Gln	Ala	Gly	Gly	Lys	



305 310 315 320

Gly Ser Asp Gly His Gln Arg Ile Leu Asp Ile Gln Pro Thr Glu Ile  
325 330 335

His Gln Arg Val Pro Leu Tyr Ile Gly Ser Val Glu Glu Val Glu Lys  
340 345 350

Leu Glu Lys Tyr Leu Ala  
355

<210> 2  
<211> 1074  
<212> DNA  
<213> Spinacia oleracea L

<220>

<223> Fructose-1,6-bisphosphatase

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gaaacactaa caggctggct gcttaaacaa gaaatggcag gtgttattga tgctgaactt 120  
accatcgttc tttctagcat ttcattggct tgtaaacaaa ttgcttcctt gggtcaacga 180  
gctgggtatth ctaacttgac tggaattcaa ggtgctgtca atatccaagg agaggatcag 240  
aagaaacttg atgttgtctc caatgaggtg ttttcgagct gcttgagatc gagtggaaga 300  
acaggaataa tagcatcaga agaagaggat gtaccagtgg cagtggaaga gaggttactct 360  
ggaaactata ttgttgtgtt tgatccactt gatgggttcat ccaacattga tgcagctgtc 420  
tccactgggtt ccatcttttg catttatagc cctaacgatg agtgcattgt tgactctgat 480  
cacgacgatg agtcacagct aagtgcagaa gaacagaggt gtgtagtgaa tgtatgtcaa 540  
ccaggggata acctattagc agcagggtat tgtatgtact caagctctgt tatcttcgta 600  
cttacaattg gtaaagggtg gtatgcattc acattagatc caatgtatgg tgaattcgta 660  
ctcacttcag agaaaatcca aatcccaaaa gctgggaaga tctattcatt caatgaaggt 720  
aactacaaaa tgtgggatga taaattgaag aagtacatgg atgatcttaa agagccagga 780  
gagtcacaga aaccgtactc gtctcgttac ataggaggtt tagttgggga ctttcataga 840  
acacttttat atggtgggat ttatgggttac ccaagagatg caaagagtaa gaatgggaaa 900  
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ggttctgatg gtcacaaag aattcttgac attcaaccca ccgagataca tcaacgtgtg 1020

ccactgtaca tcgggagtgt ggaggaagta gagaaattag agaagtactt agca 1074

<210> 3

<211> 333

<212> PRT

<213> Spinacia oleracea L

<220>

<223> Sedoheptulose-1, 7-bisphosphatase

<400> 3

Val	Asn	Lys	Ala	Lys	Asn	Ser	Ser	Leu	Val	Thr	Lys	Cys	Glu	Leu	Gly
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Asp	Ser	Leu	Glu	Glu	Phe	Leu	Ala	Lys	Ala	Thr	Thr	Asp	Lys	Gly	Leu
			20					25					30		
Ile	Arg	Leu	Met	Met	Cys	Met	Gly	Glu	Ala	Leu	Arg	Thr	Ile	Gly	Phe
		35					40					45			
Lys	Val	Arg	Thr	Ala	Ser	Cys	Gly	Gly	Thr	Gln	Cys	Val	Asn	Thr	Phe
	50					55					60				
Gly	Asp	Glu	Gln	Leu	Ala	Ile	Asp	Val	Leu	Ala	Asp	Lys	Leu	Leu	Phe
65				70						75					80
Glu	Ala	Leu	Asn	Tyr	Ser	His	Phe	Cys	Lys	Tyr	Ala	Cys	Ser	Glu	Glu
			85						90					95	
Leu	Pro	Glu	Leu	Gln	Asp	Met	Gly	Gly	Pro	Val	Asp	Gly	Gly	Phe	Ser
		100						105						110	
Val	Ala	Phe	Asp	Pro	Leu	Asp	Gly	Ser	Ser	Ile	Val	Asp	Thr	Asn	Phe
		115						120					125		
Ser	Val	Gly	Thr	Ile	Phe	Gly	Val	Trp	Pro	Gly	Asp	Lys	Leu	Thr	Gly
	130					135					140				
Val	Thr	Gly	Arg	Asp	Gln	Val	Ala	Ala	Ala	Met	Gly	Ile	Tyr	Gly	Pro
145					150					155					160

Arg Thr Thr Tyr Val Leu Ala Leu Lys Asp Tyr Pro Gly Thr His Glu  
165 170 175

Phe Leu Leu Leu Asp Glu Gly Lys Trp Gln His Val Lys Glu Thr Thr  
180 185 190

Glu Ile Asn Glu Gly Lys Leu Phe Cys Pro Gly Asn Leu Arg Ala Thr  
195 200 205

Ser Asp Asn Ala Asp Tyr Ala Lys Leu Ile Gln Tyr Tyr Ile Lys Glu  
210 215 220

Lys Tyr Thr Leu Arg Tyr Thr Gly Gly Met Val Pro Asp Val Asn Gln  
225 230 235 240

Ile Ile Val Lys Glu Lys Gly Ile Phe Thr Asn Val Ile Ser Pro Thr  
245 250 255

Ala Lys Ala Lys Leu Arg Leu Leu Phe Glu Val Ala Pro Leu Gly Phe  
260 265 270

Leu Ile Glu Lys Ala Gly Gly His Ser Ser Glu Gly Thr Lys Ser Val  
275 280 285

Leu Asp Ile Glu Val Lys Asn Leu Asp Asp Arg Thr Gln Val Ala Tyr  
290 295 300

Gly Ser Leu Asn Glu Ile Ile Arg Phe Glu Lys Thr Leu Tyr Gly Ser  
305 310 315 320

Ser Arg Leu Glu Glu Pro Val Pro Val Gly Ala Ala Ala  
325 330

<210> 4  
<211> 999  
<212> DNA  
<213> Spinacia oleracea L

<220>

<223> Sedoheptulose-1,7-bisphosphatase

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gagttcctag caaaggcaac cacagataaa gggctgatta gattgatgat gtgcatggga 120

gaagcattaa ggaccattgg ctttaaagtg aggactgctt catgtggtgg aactcaatgt 180

gttaacacct ttggagacga acagcttgcc attgatgtgc ttgctgacaa gcttccttttc 240

gaggcattga actattcaca cttctgcaag tatgcttggt cagaagaact ccctgagctt 300

caagatatgg gagggccccgt tgatggcgga ttcagtgtag catttgaccc ccttgatgga 360

tccagcattg tcgataccaa tttctcagtt gggaccatat tcgggggtttg gccagggtgac 420

aagctaactg gtgtaacagg cagagatcaa gtggctgctg caatgggaat ttatggtcct 480

aggactactt atgttctcgc tcttaaggac taccctggca cccatgaatt tcttccttctt 540

gatgaaggaa agtggcaaca tgtgaaagaa acaacagaaa tcaatgaagg aaaattgttc 600

tgtcctggaa acttgagagc cacttctgac aatgctgatt atgctaagct gattcaatac 660

tatataaaag agaaatacac attgagatac actggaggaa tggttcctga tgtaaccag 720

atcatagtga aggagaaagg tatattcaca aatgtaatat cacctacagc caaggcaaag 780

ttgaggttac tgtttgaggt agctcctcta gggttcttga ttgagaaggc tggtggtcac 840

agcagtgagg gaaccaagtc tgtgttggaac attgaagtca aaaaccttga tgacagaacc 900

caagttgctt acggctcctt gaacgagatc atccgatttg agaagacact atacggatcc 960

tctaggctag aggagccagt tcctggtgga gctgctgct 999

<210> 5

<211> 356

<212> PRT

<213> Synechococcus

<220>

<223> fructose-1,6-bisphosphatase/sedoheptulose-1,7-bisphosphatase from  
Synechococcus PCC 7942

<400> 5

Met Glu Lys Thr Ile Gly Leu Glu Ile Ile Glu Val Val Glu Gln Ala  
1 5 10 15

Ala Ile Ala Ser Ala Arg Leu Met Gly Lys Gly Glu Lys Asn Glu Ala  
20 25 30

Asp Arg Val Ala Val Glu Ala Met Arg Val Arg Met Asn Gln Val Glu  
35 40 45

Met Leu Gly Arg Ile Val Ile Gly Glu Gly Glu Arg Asp Glu Ala Pro  
50 55 60

Met Leu Tyr Ile Gly Glu Glu Val Gly Ile Tyr Arg Asp Ala Asp Lys  
65 70 75 80

Arg Ala Gly Val Pro Ala Gly Lys Leu Val Glu Ile Asp Ile Ala Val  
85 90 95

Asp Pro Cys Glu Gly Thr Asn Leu Cys Ala Tyr Gly Gln Pro Gly Ser  
100 105 110

Met Ala Val Leu Ala Ile Ser Glu Lys Gly Gly Leu Phe Ala Ala Pro  
115 120 125

Asp Phe Tyr Met Lys Lys Leu Ala Ala Pro Pro Ala Ala Lys Gly Lys  
130 135 140

Glu Thr Ser Ile Lys Ser Ala Thr Glu Asn Leu Lys Ile Leu Ser Glu  
145 150 155 160

Cys Leu Asp Arg Ala Ile Asp Glu Leu Val Val Val Val Met Asp Arg  
165 170 175

Pro Arg His Lys Glu Leu Ile Gln Glu Ile Arg Gln Ala Gly Ala Arg  
180 185 190

Val Arg Leu Ile Ser Asp Gly Asp Val Ser Ala Ala Ile Ser Cys Gly  
195 200 205

Phe Ala Gly Thr Asn Thr His Ala Leu Met Gly Ile Gly Ala Ala Pro  
210 215 220

Glu Gly Val Ile Ser Ala Ala Ala Met Arg Cys Leu Gly Gly His Phe  
225 230 235 240

Gln Gly Gln Leu Ile Tyr Asp Pro Glu Val Val Lys Thr Gly Leu Ile  
245 250 255

Gly Glu Ser Arg Glu Ser Asn Ile Ala Arg Leu Gln Glu Met Gly Ile  
260 265 270

Thr Asp Pro Asp Arg Val Tyr Asp Ala Asn Glu Leu Ala Ser Gly Gln  
275 280 285

Glu Val Leu Phe Ala Ala Cys Gly Ile Thr Pro Gly Leu Leu Met Glu  
290 295 300

Gly Val Arg Phe Phe Lys Gly Gly Ala Arg Thr Gln Ser Leu Val Ile  
305 310 315 320

Ser Ser Gln Ser Arg Thr Ala Arg Phe Val Asp Thr Val His Met Phe  
325 330 335

Asp Asp Val Lys Thr Val Ser Leu Pro Leu Ile Pro Asp Pro Lys Trp  
340 345 350

Arg Pro Glu Arg  
355

<210> 6  
<211> 1312  
<212> DNA  
<213> Synechococcus

<220>

<223> fructose-1,6-bisphosphatase/sedoheptulose-1,7-bisphosphatase from  
Synechococcus PCC 7942

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cgagattatt gaagttgtcg agcaggcagc gatcgctctg gcccgctga tgggcaaagg 180  
cgaaaagaat gaagccgatc gcgtcgcagt agaagcgatg cgggtgcgga tgaaccaagt 240  
ggaaatgctg ggccgcatcg tcatcggtga aggcgagcgc gacgaagcac cgatgctcta 300  
tateggtgaa gaagtgggca tctaccgcga tgcagacaag cgggctggcg taccggctgg 360  
caagctggtg gaaatcgaca tcgccgttga ccctgcgaa ggcaccaacc tctgcgccta 420  
cggtcagccc ggctcgatgg cagttttggc catctccgag aaaggcggcc tgtttgcagc 480  
tcccgacttc tacatgaaga aactggctgc acccccagct gccaaaggca aagagacatc 540  
aataaagtcc gcgaccgaaa acctgaaaat tctctcggaa tgtctcgatc gcgccatcga 600

tgaattggtg gtcgtggtca tggatcgtcc ccgccacaaa gagctaatacc aagagatccg 660  
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tcgcttcggt gacaccgttc acatgttcga cgatgtcaaa acgggtagcc tgccgttaat 1140  
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tgtttttcag cgaatccatt tgcgatcgtt tttcaaacc ttttttcgtc aaccttcttt 1260  
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<210> 7  
<211> 133  
<212> DNA  
<213> Nicotiana tabacum

<220>

<223> psbA promoter

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ttaaataaac caa 133

<210> 8  
<211> 159  
<212> DNA  
<213> Nicotiana tabacum

<220>

<223> rps16 terminator

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tatataactt tgtatgactt ttctcttcta tttttttgta tttcctccct ttccttttct 120

atttgtat ttttatcatt gcttccattg aattactag159

<210> 9<211> 805<212> DNA<213> Escherichia coli

<220>

<223> aadA

<400> 9gatccatggc t cgtgaagcg gttatcgccg aagtatcaac tcaactatca gaggtagttg60gcgtcatcga gcgccatctc gaaccgacgt tgctggccgt acatttgtag ggctccgcag120tggatggcgg cctgaagcca cacagtgata ttgatttgct ggttacggtg accgtaaggc180ttgatgaaac aacgcggcga gctttgatca acgacctttt ggaaacttcg gcttccctg240gagagagcga gattctccgc gctgtagaag tcaccattgt tgtgcacgac gacatcattc300cgtggcggtta tccagctaag cgcgaactgc aatttggaga atggcagcgc aatgacattc360ttgcaggtat cttcgagcca gccacgatcg acattgatct ggctatcttg ctgacaaaag420caagagaaca tagcgttgcc ttggtaggtc cagcggcgga ggaactcttt gatccggttc480ctgaacagga tctat ttgag gcgctaaatg aaaccttaac gctatggaac tcgccgcccg540actgggctgg cgatgagcga aatgtagtgc ttacgttgtc ccgcatttgg tacagcgcag600taaccggcaa aatcgcgccg aaggatgtcg ctgccgactg ggcaatggag cgctgccgg660cccagtatca gcccgtcata cttgaagcta gacaggctta tcttggacaa gaagaagatc720gcttggcctc gcgcgcagat cagttggaag aatttgtcca ctacgtgaaa ggcgagatca780ctaaggtagt tggcaaataa ctgca805

<210> 10<211> 4591<212> DNA<213> Artificial sequence

<220><223> synthetic construct

<220><223> pLD6

<400> 10



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ggaagagtat gagtattcaa catttccgtg tcgcccttat tccctttttt gcggcatttt	180
gccttcctgt ttttgctcac ccagaaacgc tggtgaaagt aaaagatgct gaagatcagt	240
tgggtgcacg agtgggttac atcgaactgg atctcaacag cggtaagatc cttgagagtt	300
ttcgccccga agaacgtttt ccaatgatga gcacttttaa agttctgcta tgtggcgcgg	360
tattatcccg tattgacgcc gggcaagagc aactcggtcg ccgcatacac tattctcaga	420
atgacttggt tgagtactca ccagtcacag aaaagcatct tacggatggc atgacagtaa	480
gagaattatg cagtgctgcc ataaccatga gtgataacac tgcggccaac ttacttctga	540
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